

09/647019
430 Rec'd PTO 26 SEP 2000

WO 99/50410

PCT/AU99/00220

- 1 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: THE VICTOR CHANG CARDIAC
RESEARCH INSTITUTE, THE
GENERAL HOSPITAL CORPORATION and
THE WALTER AND ELIZA HALL
INSTITUTE OF MEDICAL RESEARCH.
- (ii) TITLE OF INVENTION: NOVEL THERAPEUTIC MOLECULES
AND USES THEREFOR
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: DAVIES COLLISON CAVE
(B) STREET: 1 LITTLE COLLINS STREET
(C) CITY: MELBOURNE
(D) STATE: VICTORIA
(E) COUNTRY: AUSTRALIA
(F) ZIP: 3000
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: INTERNATIONAL APPLICATION
(B) FILING DATE: 26-MAR-1999
(C) CLASSIFICATION:
- (vii) PREVIOUS APPLICATION DATA:
(A) APPLICATION NUMBER: PP2634/98
(B) FILING DATE: 27-MAR-1998
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: HUGHES, DR E JOHN L
(C) REFERENCE/DOCKET NUMBER: EJH/TDO/DK
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: +61 3 9254 2777
(B) TELEFAX: +61 3 9254 2770
(C) TELEX: AA 31787

09647019-013604

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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 778 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 199..453
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GCTCTCAGGA CTGGAGAGAG ACAGAGCACT CCAGCTATTT CAGCCACATG AAAAGCACTG      60
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GTGTTTTTGC ACCTGGCCCGC CTGGGACTGT CCTCAGGCAG TAAACCAATC CAGAGAGCAG      180
GGCTAAGACC TTGTGAAT ATG TCG AAG CAG CCA ATT TCC AAC GTC AGA GCC      231
                Met Ser Lys Gln Pro Ile Ser Asn Val Arg Ala
                1             5             10
ATC CAG GCG AAT ATC AAT ATT CCA ATG GGA GCC TTT CGT CCG GGA GCT      279
Ile Gln Ala Asn Ile Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala
                15             20             25
GGG CAG CCT CCC AGA AGG AAA GAG AGT ACT CCT GAA ACT GAG GAG GGA      327
Gly Gln Pro Pro Arg Arg Lys Glu Ser Thr Pro Glu Thr Glu Glu Gly
                30             35             40
GCT CCT ACC ACC TCA GAG GAA AAG AAG CCA ATT CCT GGA ATG AAG AAA      375
Ala Pro Thr Thr Ser Glu Glu Lys Lys Pro Ile Pro Gly Met Lys Lys
                45             50             55
TTT CCA GGA CCT GTT GTC AAC TTG TCT GAG ATC CAA AAT GTT AAA AGT      423
Phe Pro Gly Pro Val Val Asn Leu Ser Glu Ile Gln Asn Val Lys Ser
                60             65             70             75
GAA CTG AAA TTT GTC CCC AAA GGT GAA CAG TAGTCGAAAG GACACAAAAG      473
Glu Leu Lys Phe Val Pro Lys Gly Glu Gln
                80             85
TTCACATTGG ATGCTTAGAA TCAGGAGATG CATTTCTGTTG ACGTGTTTTTT CCAAGGGAGA      533
AAAAACAATG GGTGAAATA AACAACTTCC TGAACATTTT ATACATTTGT ATGATGATCA      593
CAAACCTCCT GAATGCCCAA GACTCTAGCA AAAATATCCT GTTGTGTACAT TTATATTCT      653
TCCTTTTACT TGGTTGCATT TCTCACTTTA GCTACATTTT TGGCACCTTG TAGAGCAAAT      713
CAGCACACGA ATTTACAACC TGGGAAGTGT GGTTTTGAGG AGAGATGTGA TTTTATGAA      773
GGGGG      778

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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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 1           5           10           15
Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala Gly Gln Pro Pro Arg
          20           25           30
Arg Lys Glu Ser Thr Pro Glu Thr Glu Glu Gly Ala Pro Thr Thr Ser
          35           40           45
Glu Glu Lys Lys Pro Ile Pro Gly Met Lys Lys Phe Pro Gly Pro Val
          50           55           60
Val Asn Leu Ser Glu Ile Gln Asn Val Lys Ser Glu Leu Lys Phe Val
          65           70           75           80
Pro Lys Gly Glu Gln
                  85

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 887 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 185..448

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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GGTTCTCAAT ACCGGGAGAG GCACAGAGCT ATTTGAGCCA CATGAAAAGC ATCGGAATTG      60
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GCATCTGGCT GCCTGGGACT TCCCTTAGGC AGTAAACAAA TACATAAAGC AGGGATAAGA      180
CTGC ATG AAT ATG TCG AAA CAG CCA GTT TCC AAT GTT AGA GCC ATC CAG      229
  Met Asn Met Ser Lys Gln Pro Val Ser Asn Val Arg Ala Ile Gln
    1           5           10           15
GCA AAT ATC AAT ATT CCA ATG GGA GCC TTT CGG CCA GGA GCA GGT CAA      277
Ala Asn Ile Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala Gly Gln
          20           25           30
CCC CCC AGA AGA AAA GAA TGT ACT CCT GAA GTG GAG GAG GGT GTT CCT      325
Pro Pro Arg Arg Lys Glu Cys Thr Pro Glu Val Glu Glu Gly Val Pro
          35           40           45

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- 4 -

CCC ACC TCG GAT GAG GAG AAG AAG CCA ATT CCA GGA GCG AAG AAA CTT 373
Pro Thr Ser Asp Glu Glu Lys Lys Pro Ile Pro Gly Ala Lys Lys Leu
50 55 60

CCA GGA CCT GCA GTC AAT CTA TCG GAA ATC CAG AAT ATT AAA AGT GAA 421
Pro Gly Pro Ala Val Asn Leu Ser Glu Ile Gln Asn Ile Lys Ser Glu
65 70 75

CTA AAA TAT GTC CCC AAA GCT GAA CAG TAGTAGGAAG AAAAAAGGAT 468
Leu Lys Tyr Val Pro Lys Ala Glu Gln
80 85

TGATGTGAAG AAATAAAGAG GCAGAAGATG GATTCAATAG CTCCTAAAA TTTTATATAT 528

TTGTATGATG ATTGTGAACC TCCTGAATGC CTGAGACTCT AGCAGAAATG GCCTGTTTGT 588

ACATTTATAT CTCTTCCTTC TAGTTGGCTG TATTTCTTAC TTTATCTTCA TTTTGGGCAC 648

CTCACAGAAC AAATTAGCCC ATAAATTCAA CACCTGGAGG GTGTGGTTTT GAGGAGGGAT 708

ATGATTTTAT GGAGAATGAT ATGGCAATGT GCCTAACGAT TTTGATGAAA AGTTTCCCAA 768

GCTACTTCCT ACAGTATTTT GGTCAATATT TGGAAATGCGT TTTAGTTCTT CACCTTTTAA 828

ATTATGTCAC TAACTTTTGT ATGAGTTCAA ATAAATATTT GACTAAATGT AAAATGTGA 887

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asn Met Ser Lys Gln Pro Val Ser Asn Val Arg Ala Ile Gln Ala
1 5 10 15

Asn Ile Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala Gly Gln Pro
20 25 30

Pro Arg Arg Lys Glu Cys Thr Pro Glu Val Glu Glu Gly Val Pro Pro
35 40 45

Thr Ser Asp Glu Glu Lys Lys Pro Ile Pro Gly Ala Lys Lys Leu Pro
50 55 60

Gly Pro Ala Val Asn Leu Ser Glu Ile Gln Asn Ile Lys Ser Glu Leu
65 70 75 80

Lys Tyr Val Pro Lys Ala Glu Gln
85

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(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Ser Lys Gln Pro Ala Ser Asn Ile Arg Ser Ile Gln Ala Asn Ile
1          5          10          15
Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala Gly Gln Pro Pro Lys
20          25          30
Arg Lys Glu Phe Ser Thr Glu Glu Glu Gln His Val Pro Thr Pro Glu
35          40          45
Ser Glu Glu Lys Ser Glu Glu Lys Lys Pro Ile Pro Gly Ala Val Lys
50          55          60
Leu Pro Gly Pro Ala Phe Asn Leu Ser Glu Thr
65          70          75

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(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 887 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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GCATCTGGCT GCCTGGGACT TCCCTTAGGC AGTAAACAAA TACATAAAGC AG      172

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 887 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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GGATAAGACT GCATGAATAT GTCGAAACAG CCAGTTTCCA ATGTTAGAGC CATCCAG      57

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(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 887 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCAAATATCA ATATTCCAAT GGGAGCCTTT CGGCCAGGAG CAGGTCAACC CCCCAGAAGA 60
 AAAGAATGTA CTCCTGAAGT GGAGGAG 87

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 887 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGTGTTCCTC CCACCTCGGA TGAGGAGAAG AAGCCAATTC CAGGAGCGAA GAAACTTCCA 60
 GGACCTGCAG TCAATCTATC GGAAATCCAG AATATTAAAA GTGAACTAAA ATATGTCCCC 120
 AAAGCTGAAC AGTAGTAGGA AGAAAAAAG 149

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 887 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GATTGATGTG AAGAAATAAA GAGGCAGAAG ATGGATTCAA TAGCTCACTA AAATTTTATA 60
 TATTTGTATG ATGATTGTGA ACCTCCTGAA TGCCTGAGAC TCTAGCAGAA ATGGCCTGTT 120
 TGTACATTTA TATCTCTTCC TTCTAGTTGG CTGTATTTCT TACTTTATCT TCATTTTGG 180
 CACCTCACAG AACAAATTAG CCCATAAATT CAACACCTGG AGGGTGTGGT TTTGAGGAGG 240
 GATATGATTT TATGGAGAAT GATATGGCAA TGTGCCTAAC GATTTTGATG AAAAGTTTCC 300
 CAAGCTACTT CCTACAGTAT TTTGGTCAAT ATTTGGAATG CGTTTTAGTT CTTACCTTT 360
 TAAATTATGT CACTAAACTT TGTATGAGTT CAAATAAATA TTTGACTAAA TGTAAAATGT 420
 GA 422

09647049.013601

SEQUENCE LISTING

<110> Harvey, Richard P.
Palmer, Stephen J.
Rosenthal, Nadia A.
Musaro, Antonio

<120> NOVEL MOLECULES EXPRESSED DURING MUSCLE
DEVELOPMENT AND GENETIC SEQUENCES ENCODING THE SAME

<130> 12525-407001

<140> 09/647,019

<141> 2000-09-26

<150> PCT/AU99/00220

<151> 1999-03-26

<150> AU PP2634/98

<151> 1998-03-27

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1

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<221> CDS

<222> (199)...(453)

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| gaattgagat | ccccgctcag | aggacaccgg | gagttccttc | tatcctgtaa | agcgcttttt | | 120 | | | | | | | | | |
| gtgtttttgc | acctggccgc | ctgggactgt | cctcaggcag | taaaccaatc | cagagagcag | | 180 | | | | | | | | | |
| ggctaagacc | ttgtgaat | atg | tcg | aag | cag | cca | att | tcc | aac | gtc | aga | gcc | 231 | | | |
| | | Met | Ser | Lys | Gln | Pro | Ile | Ser | Asn | Val | Arg | Ala | | | | |
| | | 1 | | | | 5 | | | | | | 10 | | | | |
| atc | cag | gcg | aat | atc | aat | att | cca | atg | gga | gcc | ttt | cgt | ccg | gga | gct | 279 |
| Ile | Gln | Ala | Asn | Ile | Asn | Ile | Pro | Met | Gly | Ala | Phe | Arg | Pro | Gly | Ala | |
| | | 15 | | | | | 20 | | | | | | 25 | | | |
| ggg | cag | cct | ccc | aga | agg | aaa | gag | agt | act | cct | gaa | act | gag | gag | gga | 327 |
| Gly | Gln | Pro | Pro | Arg | Arg | Lys | Glu | Ser | Thr | Pro | Glu | Thr | Glu | Glu | Gly | |
| | | 30 | | | | | 35 | | | | | 40 | | | | |
| gct | cct | acc | acc | tca | gag | gaa | aag | aag | cca | att | cct | gga | atg | aag | aaa | 375 |
| Ala | Pro | Thr | Thr | Ser | Glu | Glu | Lys | Lys | Pro | Ile | Pro | Gly | Met | Lys | Lys | |
| | | 45 | | | | | 50 | | | | | 55 | | | | |
| ttt | cca | gga | cct | gtt | gtc | aac | ttg | tct | gag | atc | caa | aat | gtt | aaa | agt | 423 |

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Phe Pro Gly Pro Val Val Asn Leu Ser Glu Ile Gln Asn Val Lys Ser
60 65 70 75

gaa ctg aaa ttt gtc ccc aaa ggt gaa cag tagtcgaaag gacacaaaag 473
Glu Leu Lys Phe Val Pro Lys Gly Glu Gln
80 85

ttcacattgg atgcttagaa tcaggagatg catttcgttg acgtgttttt ccaagggaga 533
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tccttttact tgggtgcatt tctcacttta gctacatttt tggcaccttg tagagcaaat 713
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ggggg 778

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<213> Mus musculus

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20 25 30
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35 40 45
Glu Glu Lys Lys Pro Ile Pro Gly Met Lys Lys Phe Pro Gly Pro Val
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Val Asn Leu Ser Glu Ile Gln Asn Val Lys Ser Glu Leu Lys Phe Val
65 70 75 80
Pro Lys Gly Glu Gln
85

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ctgc atg aat atg tcg aaa cag cca gtt tcc aat gtt aga gcc atc cag 229
Met Asn Met Ser Lys Gln Pro Val Ser Asn Val Arg Ala Ile Gln
1 5 10 15

gca aat atc aat att cca atg gga gcc ttt cgg cca gga gca ggt caa 277
Ala Asn Ile Asn Ile Pro Met Gly Ala Phe Arg Pro Gly Ala Gly Gln
20 25 30

ccc ccc aga aga aaa gaa tgt act cct gaa gtg gag gag ggt gtt cct 325
Pro Pro Arg Arg Lys Glu Cys Thr Pro Glu Val Glu Glu Gly Val Pro
35 40 45

09647049.042604

ccc acc tcg gat gag gag aag aag cca att cca gga gcg aag aaa ctt 373
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cca gga cct gca gtc aat cta tcg gaa atc cag aat att aaa agt gaa 421
 Pro Gly Pro Ala Val Asn Leu Ser Glu Ile Gln Asn Ile Lys Ser Glu
 65 70 75

cta aaa tat gtc ccc aaa gct gaa cag tagtaggaag aaaaaaggat 468
 Leu Lys Tyr Val Pro Lys Ala Glu Gln
 80 85

tgatgtgaag aaataaagag gcagaagatg gattcaatag ctactaaaa ttttatatat 528
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 35 40 45
 Thr Ser Asp Glu Glu Lys Lys Pro Ile Pro Gly Ala Lys Lys Leu Pro
 50 55 60
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 Lys Tyr Val Pro Lys Ala Glu Gln
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<210> 5
 <211> 75
 <212> PRT
 <213> Xenopus laevis

<400> 5
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 aaagaatgta ctctgaagt ggaggag 87

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 tgtacattta tatctcttcc ttctagttag ctgtatttct tactttatct tcatttttgg 180
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 gatatgattt tatggagaat gatatggcaa tgtgcctaac gattttgatg aaaagtttcc 300
 caagctactt cctacagtat tttgggtcaat atttggaaat cgtttttagtt cttcaccttt 360
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 ga 422

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 <213> Patinopecten sp.

05647019.012601

<400> 11

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| Ser | Val | Ile | Gln | Arg | Asn | Ile | Arg | Lys | Trp | Val | Leu | Arg | Leu | Asn | Trp |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Gln | Trp | Trp | Lys | Leu | Tyr | Ser | Lys | Val | Lys | Pro | Leu | Leu | Ser | Ile | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Arg | Gln | Glu | Glu | Glu | Met | Lys | Glu | | | | | | | | |
| | | 35 | | | | | 40 | | | | | | | | |

<210> 12

<211> 40

<212> PRT

<213> Rattus norvegicus

<400> 12

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Val | Ile | Gln | Trp | Asn | Ile | Arg | Ala | Phe | Met | Gly | Val | Lys | Asn | Trp |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Pro | Trp | Met | Lys | Leu | Tyr | Phe | Lys | Ile | Lys | Pro | Leu | Leu | Lys | Ser | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Thr | Glu | Lys | Glu | Met | Ala | Asn | | | | | | | | |
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<210> 13

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<212> PRT

<213> Rattus norvegicus

<400> 13

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Cys | Ile | Gln | Tyr | Asn | Ile | Arg | Ala | Phe | Met | Asn | Val | Lys | His | Trp |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Pro | Trp | Met | Lys | Leu | Phe | Phe | Lys | Ile | Lys | Pro | Leu | Leu | Lys | Ser | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Thr | Glu | Lys | Glu | Met | Ala | Thr | | | | | | | | |
| | | 35 | | | | | 40 | | | | | | | | |

<210> 14

<211> 40

<212> PRT

<213> Homo sapiens

<400> 14

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| Glu | Asn | Asn | Val | Met | Asn | Ile | Arg | Gln | Phe | Asn | Cys | Ser | Pro | His | Pro |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Tyr | Trp | Leu | Pro | Asn | Phe | Met | Asp | Val | Phe | Thr | Trp | Ser | Leu | Pro | Phe |
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| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ile | Ser | Trp | Ile | Lys | Arg | Lys | Arg | Gln | Gln | | | | | | |
| | | | 20 | | | | | 25 | | | | | | | |

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